#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,461

TIME: 16:22:42

DATE: 12/26/2001

Input Set : N:\Crf3\RULE60\09879461.txt Output Set: N:\CRF3\12262001\I879461.raw

## SEQUENCE LISTING

```
ENTERED
        (1) GENERAL INFORMATION:
      5
             (i) APPLICANT: Holmes, Stephen D.
      6
                            Gross, Mitchell S.
      7
                            Sylvester, Daniel R.
      9
            (ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
     10
                                      Treatment of IL4 Mediated Disorders
           (iii) NUMBER OF SEQUENCES: 58
     12
            (iv) CORRESPONDENCE ADDRESS:
     14
     15
                  (A) ADDRESSEE: SmithKline Beecham Corporation
                  (B) STREET: Corporate Intellectual Property, UW2220 - 709
     16
     17
                               Swedeland Rd.
                  (C) CITY: King of Prussia
     18
     19
                  (D) STATE: PA
                  (E) COUNTRY: USA
     20
     21
                  (F) ZIP: 19406-2799
     23
             (V) COMPUTER READABLE FORM:
     24
                  (A) MEDIUM TYPE: Floppy disk
     25
                  (B) COMPUTER: IBM PC compatible
     26
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     27
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
     29
            (vi) CURRENT APPLICATION DATA:
C--> 30
                  (A) APPLICATION NUMBER: US/09/879,461
                  (B) FILING DATE: 12-Jun-2001
C--> 31
                  (C) CLASSIFICATION:
     32
           (vii) PRIOR APPLICATION DATA:
     34
                  (A) APPLICATION NUMBER: 08/612,929
     35
     36
                  (B) FILING DATE:
                  (A) APPLICATION NUMBER: US 08/136,783
     38
     39
                  (B) FILING DATE: 14-OCT-1993
     41
          (viii) ATTORNEY/AGENT INFORMATION:
     42
                  (A) NAME: Sutton, Jeffrey A.
                  (B) REGISTRATION NUMBER: 34,028
     43
     44
                  (C) REFERENCE/DOCKET NUMBER: P50186-2
     46
            (ix) TELECOMMUNICATION INFORMATION:
     47
                  (A) TELEPHONE: (215) 270-5024
     48
                  (B) TELEFAX: (215) 270-5090
     52 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
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                  (A) LENGTH: 396 base pairs
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                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
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                  (D) TOPOLOGY: unknown
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            (ii) MOLECULE TYPE: cDNA
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            (ix) FEATURE:
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                  (A) NAME/KEY: CDS
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(B) LOCATION: 1..396

64

RAW SEQUENCE LISTING DATE: 12/26/2001 PATENT APPLICATION: US/09/879,461 TIME: 16:22:42

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	Met																
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77	GGC	TCC	ACT	GGT	GAC	ATT	GTG	CTG	ACC	CAA	TCT	CCA	GCT	TCT	TTG	GCT	96
78	Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	${\tt Pro}$	Ala	Ser	Leu	Ala	
79				20					25					30			
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86	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	${\tt Trp}$	$\mathtt{Tyr}$	Gln	Gln	Lys	Pro	
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90	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	
91	65				;	70	•				75					80	
	GGG																288
94	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser		Ser	Gly	Thr	Asp		Thr	
95					85					90					95		
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	Leu	Asn	Ile		Pro	Val	Glu	Glu		Asp	Ala	Ala	Thr		Tyr	Cys	
99				100					105					110			204
																CTG	384
		GII	ı ser	. Asn	GIU	Asp	Pro			. Pue	s GTZ	, GT	Y GTZ	Tini	с га	s Leu	
								100					100	•			
103		3 00 0	115					120	)				125	5			206
10	5 GAA		CAAA	CGG				120	)				125	5			396
109	5 GAA 5 Glu	Il€	AAA Lys	CGG				120	)				125	5			396
10: 10: 10:	5 GAA 5 Glu 7	11e	C AAA E Lys	CGG Arg	•	O C EC	N TD						125	5			396
10: 10: 10: 11:	5 GAA 5 Glu 7	11e 130 INE	C AAA Lys ORMA	CGG Arg	FOR			NO:	2:				125	5			396
103 103 103 113	5 GAA 5 Glu 7 ) (2)	11e 130 INE	C AAA E Lys ORMA ) SE	CGG Arg TION QUEN	FOR	HARA	CTE	NO: RISTI	2: CCS:	de			125	5			396
100 100 100 110 110 111	5 GAA 5 Glu 7 ) (2) 2	11e 130 INE	C AAA Lys ORMA ) SE	CGG Arg TION QUEN A) L	FOR	HARA H: 1	CTER	NO: RISTI	2:	ds			125	5			396
100 100 100 110 110 111 111	5 GAA 5 Glu 7 0 (2) 2 3	11e 130 INE	C AAA E Lys ORMA ORMA (	CGG Arg TION QUEN A) L B) T	FOR CE C ENGI	HARA H: 1 ami	CTER .32 a .no a	NO: RISTI amino acid	2: CCS:	ds			125	5			396
10: 10: 10: 11: 11: 11: 11:	5 GAA 5 Glu 7 0 (2) 2 3	Ile 130 INE (i	C AAA Lys ORMA ) SE (	CGG Arg TION QUEN A) L B) T	FOR CE C ENGI YPE:	CHARA H: 1 ami OGY:	CTEF .32 a .no a lir	NO: RISTI amino acid acar	2: CS: aci	ds			125	5			396
109 100 110 110 113 114 115	5 GAA 5 Glu 7 (2) 2 3 4 5	116 130 INF (i	C AAA C Lys CORMA C) SE ( ( (	CGG Arg TION QUEN A) I B) T D) T	FOR CE C ENGI YPE: OPOL	HARA H: 1 ami OGY:	CTEF .32 a .no a lir pro	NO: RISTI amino acid acid acar oteir	2: CCS: aci		40: 2		125	5			396
105 106 116 116 117 117 117 117	5 GAA 5 Glu 7 (2) 2 3 4 5 7	116 130 INE (i	C AAA Lys OORMA ) SE ( ( ( ) MC	CGG Arg TION QUEN A) I B) T D) T CQUEN	FOR CENGING TOPOL	HARA H: 1 ami OGY: YPE:	CTEF. 32 a .no a lir pro	NO: RISTI amino acid acid near oteir	2: CCS: aci	ID 1					o Val	Pro	396
109 100 110 112 113 114 119 123	5 GAA 5 Glu 7 (2) 2 3 4 5 7 9	Ile 130 INE (ii (xi Glu	C AAA Lys OORMA ) SE ( ( ( ) MC	CGG Arg TION QUEN A) I B) T D) T CQUEN	FOR CENGING TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO	CHARA CH: 1 ami COGY: CYPE: CESCR	CTEF. 32 a .no a lir pro	NO: RISTI amino acid acid near oteir	2: CCS: aci	ID N	Leu					L Pro	396
109 100 110 112 113 114 115 117 122 123	5 GAA 5 Glu 7 (2) 2 3 4 5 7 7 9 Met	Ile 130 INE (ii (xi Glu	C AAAA C Lys CORMA C) SE (( () () SE 1 Thr	CGG Arg TION QUEN A) I B) T D) T DLECU QUEN	FOR CENGIA	HARA H: 1 ami OGY: YPE: DESCR	CTER 32 a no a lir pro CIPTI	NO: RISTI amino acid near oteir ON:	2: CCS: aci sEQ	ID N Va]	Leu )	ı Leı	ı Lev	ı Tr <u>p</u>	15	5	396
109 100 110 112 113 114 115 115 122 122 124	5 GAA 5 Glu 7 9 (2) 2 8 4 5 7 9 L Met 2 1 4 Gly	Ile 130 INE (ii (xi Glu	C AAAA C Lys CORMA C) SE (( () () SE 1 Thr	CGG ATION QUEN A) I B) T D) T DLECU QUEN ASp	FOR ENGT YPE: OPOL LE T CE D Thr	HARA H: 1 ami OGY: YPE: DESCR	CTER 32 a no a lir pro CIPTI	NO: RISTI amino acid near oteir ON:	2: CCS: aci SEQ Trp	ID N Va] 10	Leu )	ı Leı	ı Lev	ı Trp	15 Let		396
109 100 110 112 113 113 113 113 123 124 125	5 GAA 5 Glu 7 9 (2) 2 8 4 5 7 9 L Met 2 1 6 Gly 5	Ile 130 INE (ii (xi Glu Ser	C AAAA C Lys CORMA C) SE (( () () MC C) SE I Thr	CGG Arg TION QUEN A) I B) T DLECU QUEN Asp	FOR CE C ENGT YPE: OPOL LE T CE D Thr	HARA H: 1 ami OGY: YPE: ESCR	CTEF 32 a no a lir pro IPTI Leu	NO: RISTI amino acid near oteir ON: Leu	2: CCS: aci SEQ Trp Thr	ID N Val 10	Leu ) Ser	Leu Pro	ı Leu D Ala	ı Trp Sei 3(	15 Let	i Ala	396
109 100 110 112 113 113 113 113 123 124 125	5 GAA 5 Glu 7 9 (2) 2 8 1 5 7 9 L Met 2 1 6 Gly 5 7 Val	Ile 130 INE (ii (xi Glu Ser	C AAAA C Lys CORMA C) SE (( () () MC C) SE I Thr	CGG Arg TION QUEN A) I B) T DLECU QUEN Asp Gly CGly	FOR CE C ENGT YPE: OPOL LE T CE D Thr	HARA H: 1 ami OGY: YPE: ESCR	CTEF 32 a no a lir pro IPTI Leu	NO: RISTI amino acid near oteir ON: Leu	2: CCS: aci SEQ Trp Thr 25	ID N Val 10	Leu ) Ser	Leu Pro	ı Leu D Ala	ı Trı Sei 3( Sei	15 Let	5	396
109 100 110 111 112 113 114 115 122 123 124 125 127 128	5 GAA 5 Glu 7 9 (2) 2 8 1 5 7 9 L Met 2 1 6 Gly 5 7 Val	Ile 130 INE (ii (xi Glu Ser	C AAAA C Lys CORMA C) SE ( ( ( ) ( ) SE Thr	CGG Arg TION QUEN A) I B) T D) T CQUEN Asp Gly Gly	FOR CE C ENGT YPE: OPOL LE T CE D Thr 5	HARA H: 1 ami OGY: YPE: ESCR Ile	CTEF 32 a no a lir pro RIPTI Leu Val	NO: RISTI amino acid near oteir ON: Leu Leu Thr	2: CCS: aci SEQ Trp Thr 25	ID N Val 10 Glr	Leu Ser Cys	Let Pro	ı Led O Ala S Ala 45	ı Trı Sei 3( ı Sei	Leu Leu Glr	a Ala a Ser	396
109 100 110 111 112 113 114 115 122 123 124 125 127 128	5 GAA 5 Glu 7 7 9 (2) 8 1 1 Met 2 1 2 Gly 5 7 7 Val 8 9	Ile 130 INE (ii (xi Glu Ser	C AAAA C Lys CORMA C) SE ((() () () MC C) SE Thr Thr Thr	CGG Arg TION QUEN A) I B) T D) T CQUEN Asp Gly Gly	FOR CE C ENGT YPE: OPOL LE T CE D Thr 5	HARA H: 1 ami OGY: YPE: ESCR Ile	CTEF 32 a no a lir pro RIPTI Leu Val	NO: RISTI amino icid lear oteir ON: Leu Leu Thr	2: CCS: aci SEQ Trp Thr 25	ID N Val 10 Glr	Leu Ser Cys	Let Pro	ı Leu O Ala B Ala 45 C Glr	ı Trı Sei 3( ı Sei	Leu Leu Glr	i Ala	396
109 100 110 111 112 113 113 122 123 124 125 136 136	5 GAA 5 Glu 7 7 9 1 Met 2 1 6 Gly 5 7 Val 8	Ile 130 INE (ii (xi Glu Ser Ser Asp	C AAAA C Lys CORMA C) SE ((((((((((((((((((((((((((((((((((((	CGG Arg TION QUEN A) I B) T DLECU QUEN Asp Gly Gly Asp	FOR CE C ENGT YPE: OPOL LE T CE D Thr 5 Asp	HARA H: 1 ami OGY: YPE: PESCR Ile Arg	CTER 32 a no a lir pro RIPTI Leu Val Ala Ser	NO: RISTI amino icid lear oteir ON: Leu Leu Thr	2: CCS: Daci SEQ Trp Thr 25	ID N Val 10 Glr Ser	Leu Ser Cys	Leu Pro Lys Tyn 60	ı Leu O Ala S Ala 45 G Glr	Tri Sei 3( Sei Gli	Let General General General	a Ala a Ser	396
109 100 110 111 112 113 113 122 123 124 125 136 136	5 GAA 5 Glu 7 7 7 7 8 8 8 9 7 8 1 Gly 7 7 8 9 1 Val 8 1 Gly	Ile 130 INE (ii (xi Glu Ser Ser Asp 50 Gln	C AAAA C Lys CORMA C) SE ((((((((((((((((((((((((((((((((((((	CGG Arg TION QUEN A) I B) T DLECU QUEN Asp Gly Gly Asp	FOR CE C ENGT YPE: OPOL LE T CE D Thr 5 Asp	HARA H: 1 ami OGY: YPE: PESCR Ile Arg	CTER 32 a no a lir pro RIPTI Leu Val Ala Ser 55	NO: RISTI amino icid lear oteir ON: Leu Leu Thr	2: CCS: Daci SEQ Trp Thr 25	ID N Val 10 Glr Ser	Leu Ser Cys	Let Pro Eys Lys Tyn 60	ı Leu O Ala S Ala 45 G Glr	Tri Sei 3( Sei Gli	Let General General General	o Ala n Ser	396
109 100 110 111 112 113 113 122 123 124 130 131 134 135	5 GAA 5 Glu 7 7 7 7 8 8 8 9 7 8 1 Gly 8 7 8 9 1 Val 8 1 Gly 6 7 8 6 8 9 1 Gly 6 7 8 9 8 9 1 Gly 6 7 8 9 9 8 9 9 8 9 9 8 9 9 8 9 9 9 9 9 9	Ile 130 INE (ii (xi Glu Ser Ser Asp 50 Gln	C AAAA C Lys FORMA C) SE ((() MC C) SE Thr Thr Thr Thr Thr Thr Pro	CGG Arg TION QUEN A) I B) T D) T DLECU QUEN Asp CGly Asp Asp	FOR CE C ENGT YPE: OPOI LE T CE D Thr 5 Asp Gln	HARACH: 1 ami OGY: YPE: YPE: Ile Arg Asp	CTER 32 a no a lir pro RIPTI Leu Val Ala Ser 55	NO: RISTI amino acid near oteir ON: Leu Thr 40 Tyr i Ile	2: CCS: Daci SEQ Trp Thr 25 Ile	ID N Val 10 Glr Ser Asr	Leu Ser Cys Trp Ala	Let Pro Lys Tyn 60 Sen	ı Leu O Ala S Ala 45 Glr O Asr	ı Trp 3( Sej 6 1 Glr	Let C Let C Glr C Glr C Lys	Ala Ser Pro	396
109 100 110 111 112 113 113 122 123 124 130 131 134 135	5 GAA 5 Glu 7 9 (2) 2 3 1	Ile 130 INE (ii (xi Glu Ser Ser Asp 50 Gln	C AAAA C Lys FORMA C) SE ((() MC C) SE Thr Thr Thr Thr Thr Thr Pro	CGG Arg TION QUEN A) I B) T D) T DLECU QUEN Asp CGly Asp Asp	FOR CE C ENGT YPE: OPOI LE T CE D Thr 5 Asp Gln	HARACH: 1 ami OGY: YPE: YPE: Ile Arg Asp Leu 70 Phe	CTER 32 a no a lir pro RIPTI Leu Val Ala Ser 55	NO: RISTI amino acid near oteir ON: Leu Thr 40 Tyr i Ile	2: CCS: Daci SEQ Trp Thr 25 Ile	ID N Val 10 Glr Ser Asr	L Leu  O Ser  Cys  Trp  Ala  75  Ser	Let Pro Lys Tyn 60 Sen	ı Leu O Ala S Ala 45 Glr O Asr	ı Trp 3( Sej 6 1 Glr	Let C Let C Glr C Glr C Lys	S Ala Ser S Pro S Ser 80 E Thr	396
100 100 110 111 112 113 114 115 112 122 123 124 135 136 137 138	5 GAA 5 Glu 7 9 (2) 2 8 1 1 5 7 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Ile 130 INE (ii (xi Glu Ser Ser Asp 50 Gln	C AAAA  Lys  CORMA  COR	CGG Arg TION QUEN A) I B) T D) T DLECU QUEN Asp Cly Cly Asp Pro	FOR CE C ENGT YPE: OPOI LE T CE C Thr 5 Asp Gln Gly Lys	HARACH: 1 ami OGY: YPE: YPE: Ile Arg Asp Leu 70 Phe	CTER 32 a lir pro RIPTI Leu Val Ala Ser 55 Leu	NO: RISTI amino acid near oteir ON: Leu Thr 40 Tyr i Ile	2: CCS: Daci SEQ Trp Thr 25 C 11e	ID N Val 10 Glr Ser Asr Ala	L Leu  Cys Trp Ala 75 Ser	Let Pro	1 Leu D Ala S Ala 45 Glr D Asr	Tri Sei 3( Sei Gli Lei Asi	Let Let Control Lys Glub Phe 95	S Ala Ser S Pro S Ser 80 E Thr	396

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,461

DATE: 12/26/2001 TIME: 16:22:42

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	Glu	Tle	Lys	Arg													
147		130	•	,													
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156			(	D) T	OPOL	OGÝ:	unkı	nown									
158		(ii	) MO	LECU	LE T	YPE:	CDN	A									
160		(ix	) FE.	ATUR:	E:												
161			•	•	•	KEY:											
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164						ESCR:											
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	GAT														CCT		108
169			Asn	Arg	Leu		Ser	Ser	Leu	Leu		Leu	Ile	Val	Pro		
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	Tyr	Val	Leu	Ser		Val	Thr	Leu	Lys		Ser	GTA	Pro	GTĀ	Ile	Leu	
174	G 3. G	000	maa	<b>a.</b> a	20	am a	3 CM	ama.	3 CM	25	mam	mma	mam	000	30	ma.	204
															TTT		204
178	GTII	PIO	ser	35	THE	ьeu	ser	ьeu	40	Cys	ser	Pne	ser	45	Phe	ser	
	СТС	N.C.C	<b>እ</b> ርጥ		ССТ	А.Т.С	ССТ	стс		тсс	λ ΤΤ	ССТ	CAG		TCA	CCA	252
															Ser		232
182	пси	Der	50	DCI	Gry	ricc	GLY	55	Der	115	110	лту	60		DCI	GIY	
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190	80					85		_			90		_	_		95	
192	AGC	AAC	CAG	GTA	TTC	CTC	AAG	ATC	ACC	AGT	GTG	GAC	ACT	GCA	GAT	ACT	396
193	Ser	Asn	Gln	Val	Phe	Leu	Lys	Ile	Thr	Ser	Val	Asp	Thr	Ala	Asp	Thr	
194					100					105					110		
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	Ala	Thr			Cys	Ala	Arg			Thr	Val	Phe	Tyr	${\tt Trp}$	$\mathtt{Tyr}$	Phe	
199				115					120					125			
						GGG											483
	Asp	Val	_	Gly	Ala	Gly	Thr		Val	Thr	Val	Ser					
203			130					135					140				
	(2)					SEQ											
208		(1)				IARAC				a							
209			•			I: 14			acıc	ıs							
210 211						amir											
211		/ ; ; ;	-	-		OGY:											
413		( T T )	ION I	1EC01	ır. Ti	PE:	ρτοι	-GTII									

RAW SEQUENCE LISTING DATE: 12/26/2001 PATENT APPLICATION: US/09/879,461 TIME: 16:22:42

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223 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
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226 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
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229 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
230 65
                         70
                                              75
232 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
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                                          90
235 Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
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                                     105
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238 Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
239
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241 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
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              (C) STRANDEDNESS: double
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              (D) TOPOLOGY: unknown
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        (ii) MOLECULE TYPE: cDNA
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        (ix) FEATURE:
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              (A) NAME/KEY: CDS
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262 ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT
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263 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Trp Ile Ser
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266 GGT GCC TAC GGG
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268
                 20
271 (2) INFORMATION FOR SEQ ID NO: 6:
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              (A) LENGTH: 20 amino acids
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         (i) SEQUENCE CHARACTERISTICS:
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RAW SEQUENCE LISTING DATE: 12/26/2001 PATENT APPLICATION: US/09/879,461 TIME: 16:22:42

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294		((	C) STR	ANDEDN	ESS:	dou	ble								
295		(1	) TOP	OLOGY:	unk	nown									
297		(ii) MOI		TYPE:	CDN	A									
299		(ix) FEA													
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301		-		ATION:							,				
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307	1	010 mag		5				10					15		- <del></del>
		CAC TCC													57
		His Ser	TON T	OD 000	TD	NO .	0 -								
	(2)	INFORMAT													
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317 318		=	-	GTH: 1			actu	5							
319			-	E: ami			*								
321			-	OLOGY:					•						
323		(ii) MOI (xi) SEQ			_		2 FO .	TD N	า . ผ						
	Mat	Gly Trp									Thr	λla	Thr	Clv	
326	1	Gry 11b	Per C	ys 110 5	116	пец	FIIC	10	Val	Ата	1111	нта	15	GIY	
		His Ser		3				10					13		
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347	$\Delta TC$	ama mma													48
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349															40
349 351	Met 1 GGT	Val Leu GCC TAC	Gln T	hr Gln 5 AG GTT	Val ACC	Phe CTG	Ile AAA	Ser 10 GAG	Leu TCT	Leu GGC	Leu CCT	Trp GGG	Ile 15 ATA	Ser TTG	96
349 351 352	Met 1 GGT	Val Leu	Gln T	hr Gln 5 AG GTT	Val ACC	Phe CTG	Ile AAA	Ser 10 GAG	Leu TCT	Leu GGC	Leu CCT	Trp GGG	Ile 15 ATA	Ser TTG	
349 351 352 353	Met 1 GGT Gly	Val Leu GCC TAC Ala Tyr	Gln T GGG C Gly G 20	hr Gln 5 AG GTT ln Val	Val ACC Thr	Phe CTG Leu	Ile AAA Lys 25	Ser 10 GAG Glu	Leu TCT Ser	Leu GGC Gly	Leu CCT Pro	Trp GGG Gly 30	Ile 15 ATA Ile	Ser TTG Leu	96
349 351 352 353 355	Met 1 GGT Gly CAG	Val Leu GCC TAC Ala Tyr CCC TCC	Gln T GGG C Gly G 20 CAG A	hr Gln 5 AG GTT ln Val CC CTC	Val ACC Thr	Phe CTG Leu CTG	Ile AAA Lys 25 ACT	Ser 10 GAG Glu TGT	Leu TCT Ser TCT	Leu GGC Gly TTC	Leu CCT Pro TCT	Trp GGG Gly 30 GGG	Ile 15 ATA Ile TTT	Ser TTG Leu TCA	
349 351 352 353 355 356	Met 1 GGT Gly CAG	Val Leu GCC TAC Ala Tyr CCC TCC Pro Ser	Gln T GGG C Gly G 20 CAG A	hr Gln 5 AG GTT ln Val CC CTC	Val ACC Thr	Phe CTG Leu CTG Leu	Ile AAA Lys 25 ACT	Ser 10 GAG Glu TGT	Leu TCT Ser TCT	Leu GGC Gly TTC	CCT Pro TCT Ser	Trp GGG Gly 30 GGG	Ile 15 ATA Ile TTT	Ser TTG Leu TCA	96
349 351 352 353 355 356 357	Met 1 GGT Gly CAG Gln	Val Leu GCC TAC Ala Tyr CCC TCC Pro Ser 35	Gln T GGG C Gly G 20 CAG A Gln T	hr Gln 5 AG GTT ln Val CC CTC hr Leu	Val ACC Thr AGT Ser	Phe CTG Leu CTG Leu 40	Ile AAA Lys 25 ACT Thr	Ser 10 GAG Glu TGT Cys	TCT Ser TCT Ser	GGC Gly TTC Phe	CCT Pro TCT Ser 45	GGG Gly 30 GGG Gly	Ile 15 ATA Ile TTT Phe	Ser TTG Leu TCA Ser	96 144
349 351 352 353 355 356 357 359	Met 1 GGT Gly CAG Gln	Val Leu GCC TAC Ala Tyr CCC TCC Pro Ser 35 AGC ACT	Gln T GGG C Gly G 20 CAG A Gln T	hr Gln 5 AG GTT ln Val CC CTC hr Leu GT ATG	ACC Thr AGT Ser	Phe CTG Leu CTG Leu 40 GTG	AAA Lys 25 ACT Thr	Ser 10 GAG Glu TGT Cys	TCT Ser TCT Ser ATT	GGC Gly TTC Phe	CCT Pro TCT Ser 45 CAG	Trp  GGG Gly 30 GGG Gly CCT	Ile 15 ATA Ile TTT Phe	TTG Leu TCA Ser	96
349 351 352 353 355 356 357 359 360	Met 1 GGT Gly CAG Gln	Val Leu GCC TAC Ala Tyr  CCC TCC Pro Ser 35 AGC ACT Ser Thr	Gln T GGG C Gly G 20 CAG A Gln T	hr Gln 5 AG GTT ln Val CC CTC hr Leu GT ATG	ACC Thr AGT Ser GGT Gly	Phe CTG Leu CTG Leu 40 GTG	AAA Lys 25 ACT Thr	Ser 10 GAG Glu TGT Cys	TCT Ser TCT Ser ATT	GGC Gly TTC Phe CGT Arg	CCT Pro TCT Ser 45 CAG	Trp  GGG Gly 30 GGG Gly CCT	Ile 15 ATA Ile TTT Phe	TTG Leu TCA Ser	96 144
349 351 352 353 355 356 357 359 360 361	Met 1 GGT Gly CAG Gln CTG Leu	Val Leu GCC TAC Ala Tyr CCC TCC Pro Ser 35 AGC ACT Ser Thr 50	Gln T GGG C Gly G 20 CAG A Gln T TCT G Ser G	hr Gln 5 AG GTT ln Val CC CTC hr Leu GT ATG ly Met	ACC Thr AGT Ser GGT Gly 55	CTG Leu CTG Leu 40 GTG Val	AAA Lys 25 ACT Thr AGC	Ser 10 GAG Glu TGT Cys TGG Trp	TCT Ser TCT Ser ATT	GGC Gly TTC Phe CGT Arg 60	CCT Pro TCT Ser 45 CAG Gln	GGG Gly 30 GGG Gly CCT Pro	Ile 15 ATA Ile TTT Phe TCA Ser	TTG Leu TCA Ser GGA Gly	96 144 192
349 351 352 353 355 356 357 359 360 361 363	Met 1 GGT Gly CAG Gln CTG Leu	Val Leu GCC TAC Ala Tyr  CCC TCC Pro Ser 35 AGC ACT Ser Thr	Gln T GGG C Gly G 20 CAG A Gln T TCT G Ser G	hr Gln 5 AG GTT ln Val CC CTC hr Leu GT ATG ly Met	ACC Thr AGT Ser GGT Gly 55 GCA	Phe CTG Leu CTG Leu 40 GTG Val	AAA Lys 25 ACT Thr AGC Ser	Ser 10 GAG Glu TGT Cys TGG Trp	TCT Ser TCT Ser ATT Ile	GGC Gly TTC Phe CGT Arg 60 GAT	CCT Pro TCT Ser 45 CAG Gln	GGG Gly 30 GGG Gly CCT Pro	Ile 15 ATA Ile TTT Phe TCA Ser	TTG Leu TCA Ser GGA Gly	96 144

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/879,461

DATE: 12/26/2001

TIME: 16:22:43

Input Set : N:\Crf3\RULE60\09879461.txt
Output Set: N:\CRF3\12262001\1879461.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]